

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

EFS

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/578,839A
Source: IFWO
Date Processed by STIC: 2/26/07

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/578,839A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
 Wrapped Aminos was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will
 prevent "wrapping."

- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

- 3 Misaligned Amino The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers;
 Numbering use **space characters**, instead.

- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please
 ensure your subsequent submission is saved in ASCII text.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules,**
 each n or Xaa can only represent a single residue. Please present the **maximum** number of each
 residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
 "bug" sequences(s) . Normally, PatentIn would automatically generate this section from the
 previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
 the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for**
 Artificial or Unknown sequences.

- 7 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

- 8 Skipped Sequences Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 (NEW RULES) <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
 (NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

- 10 Invalid <213> Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
 Response scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or
 is Artificial Sequence. (see item 11 below)

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use
 of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown."
 Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as
 explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of
 Sequence Rules

- 12 PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
 "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
 listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWO

RAW SEQUENCE LISTING

DATE: 02/26/2007

PATENT APPLICATION: US/10/578,839A

TIME: 14:32:39

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Output Set: N:\CRF4\02262007\J578839A.raw

3 <110> APPLICANT: INJE UNIVERSITY
 5 <120> TITLE OF INVENTION: CANCER CELL TARGETING GENE DELIVERY METHOD
 7 <130> FILE REFERENCE: Q94769
 9 <140> CURRENT APPLICATION NUMBER: US 10/578,839A
 10 <141> CURRENT FILING DATE: 2006-05-10
 12 <150> PRIOR APPLICATION NUMBER: KR 10-2003-0079897
 13 <151> PRIOR FILING DATE: 2003-11-12
 15 <150> PRIOR APPLICATION NUMBER: PCT/KR2004/000545
 16 <151> PRIOR FILING DATE: 2004-03-15
 18 <160> NUMBER OF SEQ ID NOS: 11
 20 <170> SOFTWARE: KopatentIn 1.71
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 36
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Artificial Sequence
 27 <220> FEATURE:
 28 <223> OTHER INFORMATION: Env F primer
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 32 cgcgatccg aattccatac ctggtgttgc tgacta 36
 35 <210> SEQ ID NO: 2
 36 <211> LENGTH: 47
 37 <212> TYPE: DNA
 38 <213> ORGANISM: Artificial Sequence
 40 <220> FEATURE:
 41 <223> OTHER INFORMATION: 597LN primer
 44 <400> SEQUENCE: 2
 45 agctggacct ggctgccacc acctccgcta ttttgggtccc attttac 47
 48 <210> SEQ ID NO: 3
 49 <211> LENGTH: 49
 50 <212> TYPE: DNA
 51 <213> ORGANISM: Artificial Sequence
 53 <220> FEATURE:
 54 <223> OTHER INFORMATION: LC597 primer
 57 <400> SEQUENCE: 3
 58 caaccccgcc gcaggtggag gaggcagtga atggactcaa aaatttcaa 49
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 62 <211> LENGTH: 35
 63 <212> TYPE: DNA
 64 <213> ORGANISM: Artificial Sequence
 66 <220> FEATURE:
 67 <223> OTHER INFORMATION: Spike R2 primer
 70 <400> SEQUENCE: 4
 71 tgctctagaa ttcttaaagg ttaccttcgt tctct 35

see pg 3-4

**Does Not Comply
Corrected Diskette Needed**

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74 <210> SEQ ID NO: 5
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79 <220> FEATURE:
80 <223> OTHER INFORMATION: LnkNScFv primer
83 <400> SEQUENCE: 5
84 ggaggtggtg gcagccaggt ccagctagtg cagtct 36
87 <210> SEQ ID NO: 6
88 <211> LENGTH: 36
89 <212> TYPE: DNA
90 <213> ORGANISM: Artificial Sequence
92 <220> FEATURE:
93 <223> OTHER INFORMATION: ScFvLnkC primer
96 <400> SEQUENCE: 6
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100 <210> SEQ ID NO: 7
101 <211> LENGTH: 2058
102 <212> TYPE: DNA
103 <213> ORGANISM: Gibbon Ape leukemia virus
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106 <221> NAME/KEY: sig_peptide
107 <222> LOCATION: (1)..(126)
109 <220> FEATURE:
110 <221> NAME/KEY: misc_feature
111 <222> LOCATION: (127)..(1467)
112 <223> OTHER INFORMATION: surface subunit region
115 <220> FEATURE:
116 <221> NAME/KEY: misc_feature
117 <222> LOCATION: (1468)..(2025)
118 <223> OTHER INFORMATION: transmembrane domain
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124 atgagtcctg ggagctggaa aagactgac atcctcttaa gctgcgtatt cggcggcgcc 120
126 gggacgagtc tgcaaaataa gaacccccac cagcccatga ccctcacttg gcaggtactg 180
128 tcccaaactg gagacgttgt ctgggataca aaggcagtc agcccccttg gacttggttg 240
130 cccacactta aacctgatgt atgtgccttg gcggctagtc ttgagtcctg ggatatcccg 300
132 ggaaccgatg tctcgtcctc taaacgagtc agacctccgg actcagacta tactgccgct 360
134 tataagcaaa tcacctgggg agccataggg tgcagctacc ctgaggctag gactagaatg 420
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138 tgcggggggc tagaatccct atactgtaaa gaatgggatt gtgagaccac ggggaccggt 540
140 tattggctat ctaaatacctc aaaagacctc ataactgtaa aatgggacca aaatagcgaa 600
142 tggactcaaa aatttcaaca gtgtcaccag accggctggt gtaaccccct taaaatagat 660
144 ttcacagaca aaggaaaatt atccaaggac tggataacgg gaaaaacctg gggattaaga 720
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148 ccagctgtgt cagtaggctc tgacctcgtc cttgtggaac aaggacctcc tagaacgtcc 840
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160 gaccgggtgcc gctggggggac ccaaggaaaag ctcaccctca ctgaggtctc aggacacggg 1200
162 ttgtgcatag gaaagggtgcc ctttaccat cagcatctct gcaatcagac cctatccatc 1260
164 aattcctccg gagaccatca gtatctgctc cctccaacc atagctggtg ggcttgacgc 1320
166 actggcctca ccccttgctc ctccacctca gtttttaate agactagaga tttctgtatc 1380
168 cagggtccagc tgattcctcg catctattac tatcctgaag aagttttgtt acaggcctat 1440
170 gacaattctc accccaggac taaaagagag gctgtctcac ttaccctagc tgttttactg 1500
172 ggggtgggaa tcacggcggg aataggctact ggttcaactg ccttaattaa aggacctata 1560
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176 caagactcag tcagcaagtt agaggactca ctgacttccc tgtccgaggt agtgctccaa 1680
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180 gaagagtgtc gtttttacat agaccactca ggtgcagtac gggactccat gaaaaaactc 1800
182 aaagaaaaac tggataaaag acagttagag cgccagaaaa gccaaaactg gtatgaagga 1860
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186 ctctccttc tgttgctcat cctcgggcca tgcctcatca ataagttagt tcaattcatc 1980
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190 aacgaaggta acctttaa 2058

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193 <210> SEQ ID NO: 8

194 <211> LENGTH: 786

195 <212> TYPE: DNA

196 <213> ORGANISM: Artificial sequence

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199 <221> NAME/KEY: misc_feature

200 <222> LOCATION: (346)..(390)

201 <223> OTHER INFORMATION: (Gly4Ser)3 linker

204 <220> FEATURE:

205 <221> NAME/KEY: misc_feature

206 <222> LOCATION: (739)..(777)

207 <223> OTHER INFORMATION: PreS1 Tag

210 <400> SEQUENCE: 8

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215 cctggacaac gccttgagtg gatgggatat ttttctctg gcaacgatga ttttaaatac 180
217 tcccagaagt tccaggagcg cgtgacaatc actgcagaca aatccgagag cacagcctac 240
219 atggagctga gcagcctgag atctgaggac acggcggtct attactgtgc aagatcggtg 300
221 aacatggcat actggggcca agggactctg gtcactgtct cttcagggtg aggcggttca 360
223 ggccggaggtg gctctggcgg tggcggatcg gacattgtga tgaccagtc tccagactcc 420
225 ctggctgtgt ctctgggcga gagggccacc atcaactgca agtccagcca gagtgtttta 480
227 tacagcagca acaataagaa ctacttagct tggtagcagc agaaaccagg acagcctctc 540
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231 agcgggtctg ggacagattt cactctcacc atcagcagcc tgcaggctga agatgtggca 660
233 gtttattact gtcagcaata ttattcctat ccggtgacgt tcggccaagg gaccaagggtg 720
235 gaaatcaaag cggccgcagg agccaacgca aacaatccag attgggactt caaccccgcc 780
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240 <210> SEQ ID NO: 9

241 <211> LENGTH: 13

242 <212> TYPE: PRT

243 <213> ORGANISM: PreS1 epitope at C-terminal of Tag-72pS1

*this is not entirely explained**what about locations 1-345, 391-738, 778-786?**they need explanation**what is (are) their source(s)? see item 11 on Enr summary sheet**invalid <213> response (see item 10 on Enr summary sheet)*

RAW SEQUENCE LISTING

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247 1 5 10

250 <210> SEQ ID NO: 10

251 <211> LENGTH: 2871

252 <212> TYPE: DNA

253 <213> ORGANISM: Artificial Sequence

255 <220> FEATURE:

256 <223> OTHER INFORMATION: ScFv-GaLV Env GP chimeric peptide (FvGEL199) DNA

259 <400> SEQUENCE: 10

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264 gggacgagtc tgcaaaataa gaacccccac cagcccatga ccctcacttg gcaggtagtg 180
266 tcccaactg gagacgttgt ctgggataca aaggcagtc agcccccttg gacttggtgg 240
268 cccacactta aacctgatgt atgtgccttg gcggctagtc ttgagtcctg ggatatcccg 300
270 ggaaccgatg tctcgtcttc taaacgagtc agacctccgg actcagacta tactgccgct 360
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276 tgcggggggc tagaatccct atactgtaaa gaatgggatt gtgagaccac ggggaccggg 540
278 tattggctat ctaaatectc aaaagacctc ataactgtaa aatgggacca aaatagcgga 600
280 ggtggtggca gccagggtcca gctagtgcag tctggggctg aagtgaagaa gcctggggct 660
282 tcagtgaagg tgcctgcaa ggcttctggc tacaccttca ctgaccatgc aattcactgg 720
284 gtgcgccagg cccctggaca acgccttgag tggatgggat atttttctcc tggcaacgat 780
286 gattttaaat actcccagaa gttccaggga cgcgtgacaa tcaactgcga caaatcccg 840
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296 cagagtgttt tatacagcag caacaataag aactacttag cttggtacca gcagaaacca 1140
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326 aagctcacc tcactgaggt ctcaggacac ggggtgtgca taggaaaggt gccctttacc 2040
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330 ctcccccca accatagctg gtgggcttgc agcactggcc tcaccccttg cctctccacc 2160
332 tcagttttta atcagactag agatttctgt atccagggtc agctgattcc tcgcatctat 2220
334 tactatctct aagaagtttt gttacaggcc tatgacaatt ctacccccag gactaaaaga 2280
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 Output Set: N:\CRF4\02262007\J578839A.raw

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342 tcaactgactt ccctgtccga ggtagtgtc caaaatagga gaggccttga cttgctgttt 2520
344 ctaaaagaag gtggcctctg tgcggcccta aaggaagagt gctgttttta catagaccac 2580
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348 gagcgccaga aaagccaaaa ctggtatgaa ggatggttca ataactcccc ttggttctact 2700
350 accctgctat caaccatcgc tgggccccta ttactcctcc ttctgttgct catcctcggg 2760
352 ccatgcatca tcaataagtt agttcaattc atcaatgata ggataagtgc agttaaatt 2820
354 ctggtcctta gacaaaaata tcaggcccta gagaacgaag gtaaccttta a 2871
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359 <212> TYPE: PRT
360 <213> ORGANISM: Artificial Sequence
362 <220> FEATURE:
363 <223> OTHER INFORMATION: ScFv-GaLV Env GP chimeric ligand (FvGEL199)
366 <400> SEQUENCE: 11
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371 20 25 30
373 Leu Ser Cys Val Phe Gly Gly Gly Gly Thr Ser Leu Gln Asn Lys Asn
374 35 40 45
376 Pro His Gln Pro Met Thr Leu Thr Trp Gln Val Leu Ser Gln Thr Gly
377 50 55 60
379 Asp Val Val Trp Asp Thr Lys Ala Val Gln Pro Pro Trp Thr Trp Trp
380 65 70 75 80
382 Pro Thr Leu Lys Pro Asp Val Cys Ala Leu Ala Ala Ser Leu Glu Ser
383 85 90 95
385 Trp Asp Ile Pro Gly Thr Asp Val Ser Ser Ser Lys Arg Val Arg Pro
386 100 105 110
388 Pro Asp Ser Asp Tyr Thr Ala Ala Tyr Lys Gln Ile Thr Trp Gly Ala
389 115 120 125
391 Ile Gly Cys Ser Tyr Pro Arg Ala Arg Thr Arg Met Ala Ser Ser Thr
392 130 135 140
394 Phe Tyr Val Cys Pro Arg Asp Gly Arg Thr Leu Ser Glu Ala Arg Arg
395 145 150 155 160
397 Cys Gly Gly Leu Glu Ser Leu Tyr Cys Lys Glu Trp Asp Cys Glu Thr
398 165 170 175
400 Thr Gly Thr Gly Tyr Trp Leu Ser Lys Ser Ser Lys Asp Leu Ile Thr
401 180 185 190
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406 Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
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409 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His Ala Ile His Trp
410 225 230 235 240
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VERIFICATION SUMMARY

DATE: 02/26/2007

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TIME: 14:32:40

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